Progress in Virus Resistance Breeding in Uganda

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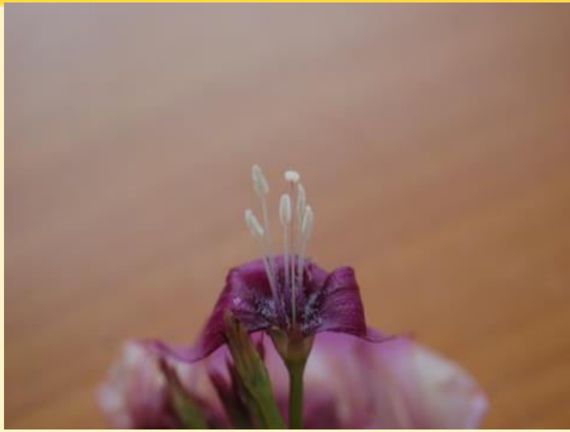
Outline of presentation

- Background, Yield losses due to swetpotato virus disease (SPVD)
- Old breeding cycle
- Progress to date



Sweetpotato Virus Disease (SPVD) Causes Significant Yield Losses (50->90%)

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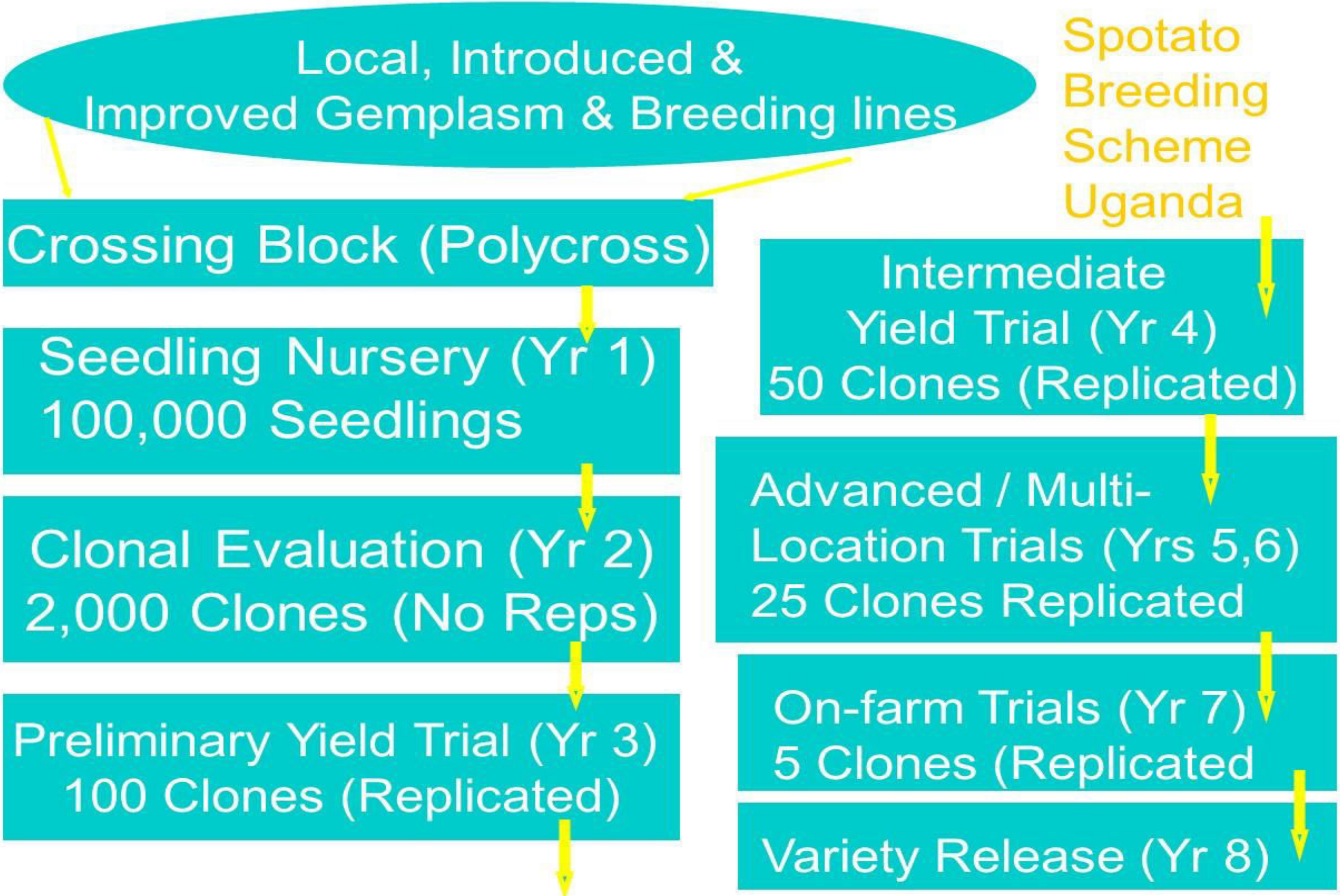
Clark et al. 2012: Plant Disease

Spotato Breeding Scheme Uganda



Local, Introduced & Improved Gemplasm & Breeding lines

Crossing Block (Polycross)

Seedling Nursery (Yr 1)
100,000 Seedlings

Clonal Evaluation (Yr 2)
2,000 Clones (No Reps)

Preliminary Yield Trial (Yr 3)
100 Clones (Replicated)

Intermediate Yield Trial (Yr 4)
50 Clones (Replicated)

Advanced / Multi-Location Trials (Yrs 5,6)
25 Clones Replicated

On-farm Trials (Yr 7)
5 Clones (Replicated

Variety Release (Yr 8)

Table 1. Sweetpotato varieties released in Uganda 1995 to date (Mwanga et al. 2016, HortScience, 51)

Year released	Cultivar/comment	No of cultivars
1995	Bwanjule, New Kawogo, Tanzania, Wagabolige, Sowola, Tororo 3	6
1999	NASPOT 1 to NASPOT 6	6
2004	Ejumula, Kakamega /orange-fleshed	2
2007	NASPOT 7, NASPOT 8, NASPOT 9 O (Vita), NASPOT 10 O (Kabode), Dimbuka-Bukulula	5
2010	NASPOT 11 / participatory breeding	1
2013	NASPOT 12 O, NASPOT 13 O	2
Total		**22**

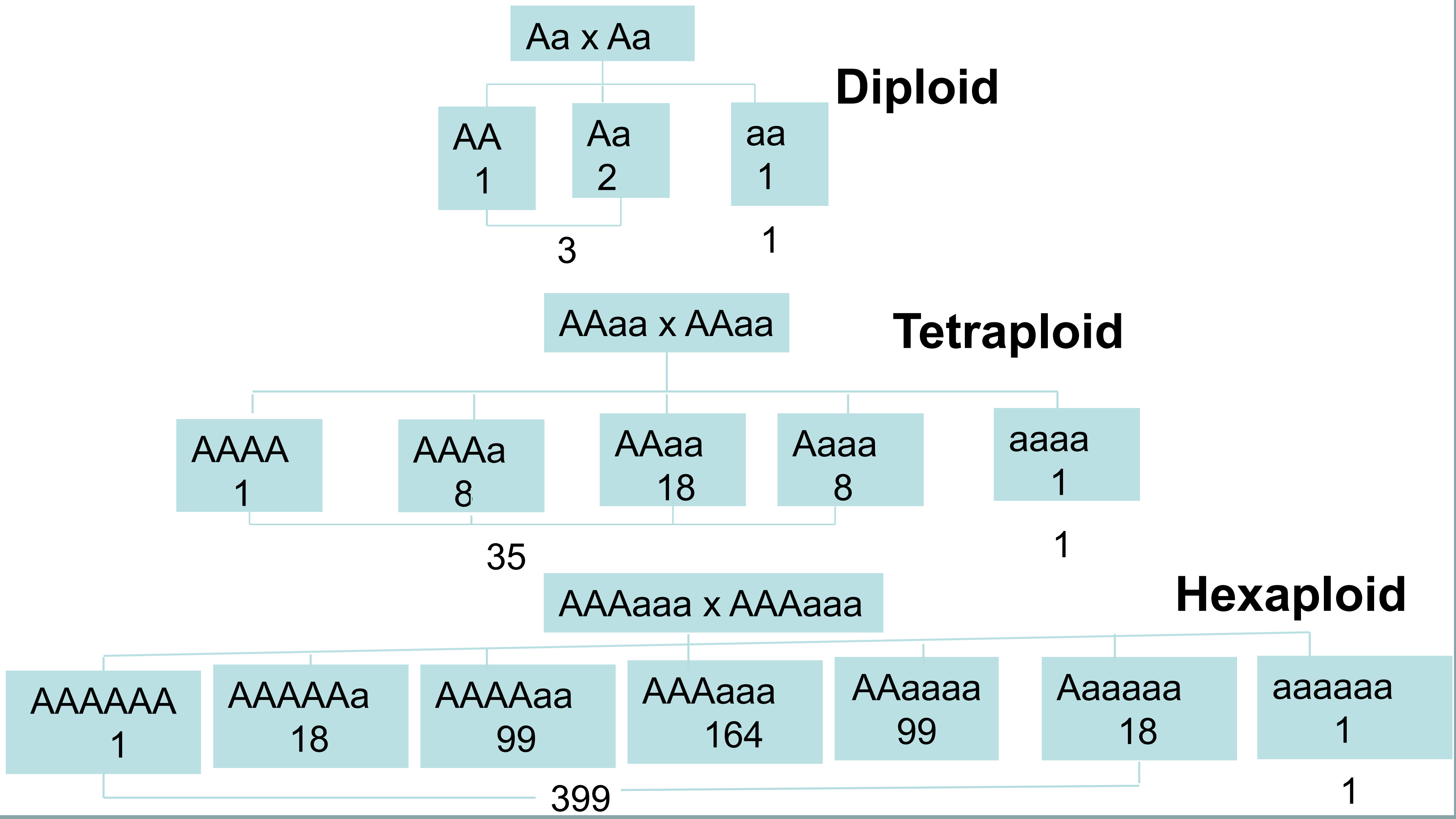
Table 2 . Origin/ main attributes of 24 sweetpotato parents used in the 2001/2002 polycross nursery at Namulonge, Uganda: (NASPOT 7 TO 10) /2007 release

Code	Female parent	Origin of parent	Year released/ status/ germplasm (GM)	Desirable / undesirable trait
1	Kala	Uganda (landrace)	GM	Orange-fleshed (OF), high dry matter (HDM)
2	NASPOT 4	Uganda (bred clone)	1999	Resistant to sweetpotao virus disease (SPVD)
3	Kanyasi	Uganda (landrace)	GM	HDM, susceptible to Alternaria blight (AB)
4	Zapallo (420027)	CIP / Peru	GM	OF, moderate resistance to AB, susceptible to SPVD
5	Ejumula	Uganda (landrace)	2004	OF, HDM, highly susceptible to SPVD
6	NASPOT 5	Uganda (bred clone)	1999	OF, HDM, resistant to SPVD, susceptible to AB
7	New Kawogo	Uganda (landrace)	1995	HDM, resistant to SPVD, susceptible to AB

Table 2. Origin and main attributes of 24 sweetpotato parents used in the 2001/2002 polycross nursery at Namulonge, Uganda (complete)

Code	Female parent	Origin of parent	Year released/ status/ germplasm (GM)	Desirable / undesirable trait
1	Kala	Uganda (landrace)	GM	Orange-fleshed (OF), high dry matter (HDM)
2	NASPOT 4	Uganda (bred clone)	1999	Resistant to sweetpotao virus disease (SPVD)
3	Kanyasi	Uganda (landrace)	GM	HDM, susceptible to Altemaria blight (AB)
4	Zapallo (420027)	CIP / Peru	GM	OF, moderate resistance to AB, susceptible to SPVD
5	Ejumula	Uganda (landrace)	2004	OF, HDM, highly susceptible to SPVD
6	NASPOT 5	Uganda (bred clone)	1999	OF, HDM, resistant to SPVD, susceptible to AB
7	New Kawogo	Uganda (landrace)	1995	HDM, resistant to SPVD, susceptible to AB
8	Bwanjule	Uganda (landrace)	1995	HDM, resistant to SPVD
9	Sowola	Uganda (landrace)	1995	HDM, early maturity, light canopy
10	Tanzania	Uganda (landrace)	1995	HDM, taste, moderately resistant to SPVD
11	NASPOT 3	Uganda (bred clone)	1999	HDM, moderately resistant to SPVD
12	Beauregard (44013)	CIP / Peru	GM	OF, good root shape, susceptible to SPVD
13	Jewel (440132)	CIP / Peru	GM	OF, susceptible to SPVD
14	NIS/199/23/60	Uganda (bred clone)	Breeding line	OF, susceptible to SPVD
15	NIS/93/29	Uganda (bred clone)	Breeding line	HDM, resistant to SPVD
16	NIS/199/18/1	Uganda (bred clone)	Breeding line	OF, susceptible to SPVD
17	NIS/199/4/4	Uganda (bred clone)	Breeding line	OF, HDM, susceptible to SPVD
18	NIS/1990/Sowola-6	Uganda (bred clone)	Breeding line	OF, susceptible to SPVD
19	Ngujja	Uganda (landrace)	GM	OF, susceptible to SPVD
20	Arivumaku-2	Uganda (landrace)	GM	OF, low root yield
21	Bunduguza	Uganda (landrace)	GM	HDM, resistance to sweetpotato weevil
22	Araka	Uganda (landrace)	GM	Adapted to short grassland area
23	SPK004 (Kakamega)	Kenya	2004	OF, HDM, moderately resistant to SPVD
24	NASPOT 1	Uganda (bred clone)	1999	OF, HDM, high root yield, susceptible to AB

Fig. 1. Segregation of dominant and recessive genotypes in di-, tetra-, and hexaploid



Aa x Aa

Diploid

AA
1

Aa
2

aa
1

3

1

AAaa x AAaa

Tetraploid

AAAA
1

AAAa
8

AAaa
18

Aaaa
8

aaaa
1

35

1

AAAaaa x AAAaaa

Hexaploid

AAAAAA
1

AAAAAa
18

AAAAaa
99

AAAaaa
164

AAaaaa
99

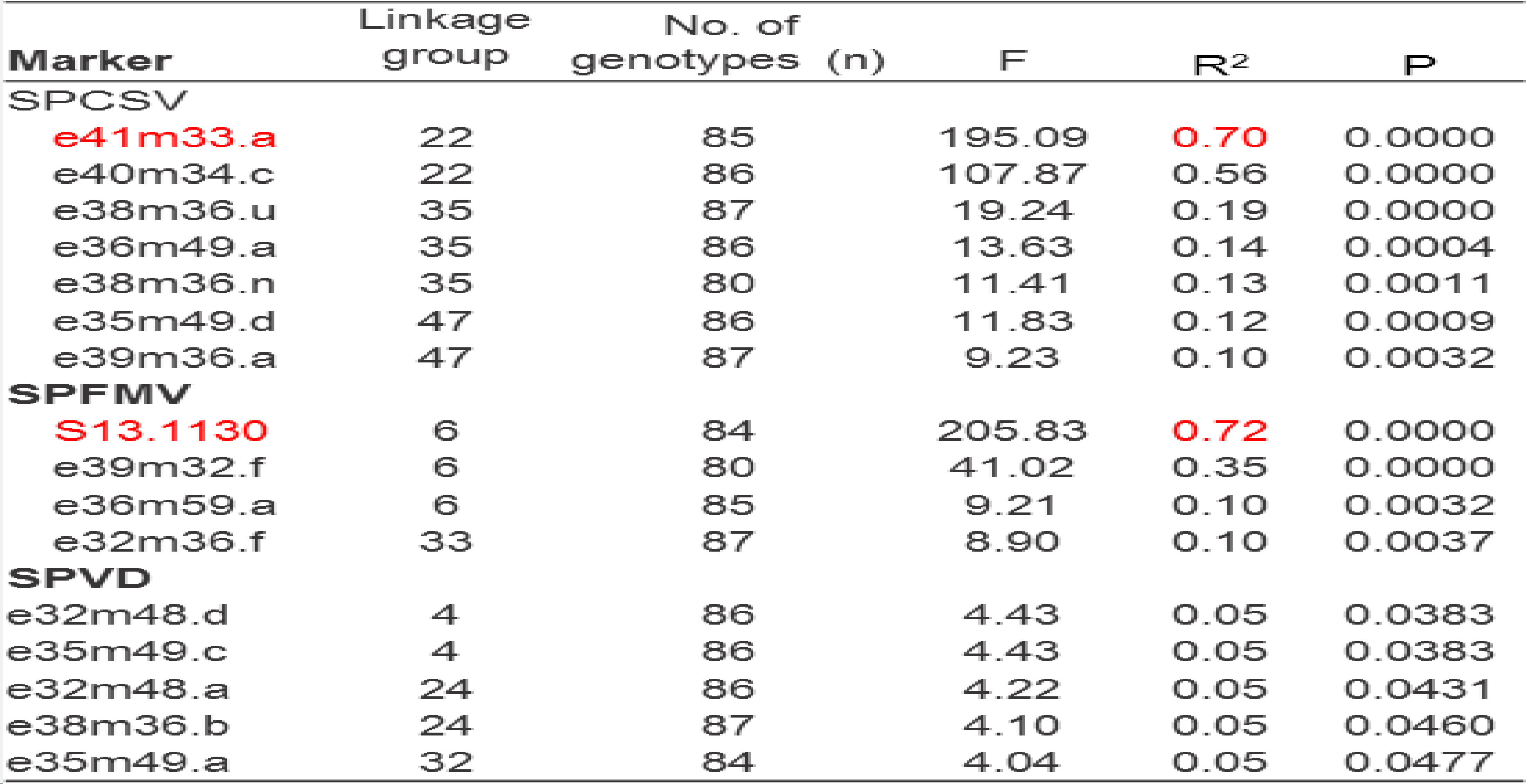
Aaaaaa
18

aaaaaa
1

399

1

Table 3. AFLP and RAPD markers associated with ≥ 10% resistance to *SP chlorotic stunt virus* (SPCSV) and *SP feathery mottle virus* (SPFMV), and ≥ 5% of the variability in resistance to SPVD in the ‘Tanzania’ x ‘Wagabolige’ cross. S13.1130 is a RAPD marker, all others are AFLP markers.



Marker	Linkage group	No. of genotypes (n)	F	R^2	P
SPCSV					
e41m33.a	22	85	195.09	0.70	0.0000
e40m34.c	22	86	107.87	0.56	0.0000
e38m36.u	35	87	19.24	0.19	0.0000
e36m49.a	35	86	13.63	0.14	0.0004
e38m36.n	35	80	11.41	0.13	0.0011
e35m49.d	47	86	11.83	0.12	0.0009
e39m36.a	47	87	9.23	0.10	0.0032
SPFMV					
S13.1130	6	84	205.83	0.72	0.0000
e39m32.f	6	80	41.02	0.35	0.0000
e36m59.a	6	85	9.21	0.10	0.0032
e32m36.f	33	87	8.90	0.10	0.0037
SPVD					
e32m48.d	4	86	4.43	0.05	0.0383
e35m49.c	4	86	4.43	0.05	0.0383
e32m48.a	24	86	4.22	0.05	0.0431
e38m36.b	24	87	4.10	0.05	0.0460
e35m49.a	32	84	4.04	0.05	0.0477

Table 4. Phenotypic ratios (resistant/ susceptible) in testcrosses for virus resistance genes (4 cytological hypotheses, assuming sp genomic constitution is R1R1R2R2R2R2 (R = dominant, r = recessive), (Jones, 1967, Kumagai et al.(1990) (Mwanga et al. 2002)

Gene	**Hypothesis 1**	**Hypotheses 2**		**Hypothesis 4**
		Hypothesis 2	**Hypothesis 3**	
	Autohexaploid (hexasomic) non preferential pairing , R1 = R2	Tetradisomic Strict preferential for R1, R2; genes on R1 have disomic inheritance, genes on R2 tetrasomic	Tetrasomic Alleles for located on R2 genome	Allohexaploid (disomic) Allele for resistance located on R1
Simplex	Rrrrrr 1:1	Rrrr rr	1:1	Rr rr rr 1:1
		Rrrr Rr	1:1	
Duplex	RRrrrr 4:1	RRrr rr	5:1	Rr Rr rr 3:1
		Rrrr Rr	3:1	RR rr rr 1:0
		Rrrr RR	1:0	
Triplex	RRRrrr 19:1	RRRr rr	1:0	Rr Rr 7:1
		RRrr Rr	11:1	RR Rr 1:0
		Rrrr RR	1:0	
Quadruplex	RRRRr 1:0	RRRR rr	1:0	RR Rr 1:0

FM/CS: TZxWAG/ TXBKM

FM:TZxWAG/ TZxBKM

SPFMV:TZxBKM

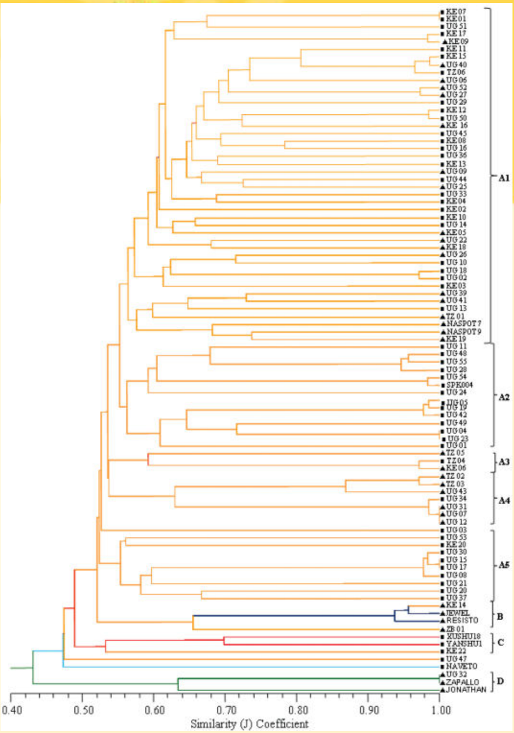
FM:TZxBKM

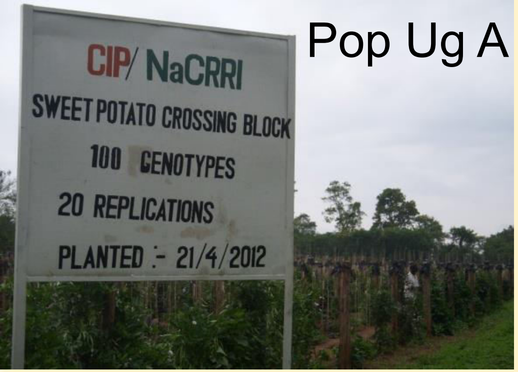
Inheritance of SPFMV and SPCSV resistance

- Dominance effects for SPCSV and SPFMV resistance genes were ruled out
- At least 50% of all progenies derived from the resistant parent would be resistant regardless of the model of inheritance (disomic, tetrasomic, tetradisomic, hexasomic)
- Exact allelic frequencies or dosage effects could not be estimated in this study
- Data suggest that the frequency of resistant SPFMV and SPCSV alleles is high, the resistant phenotypes are not as common due to the **polysomic** nature of sweetpotato and the **traits** being **recessive**

Developing populations for SPVD resistance and quality traits

- Two distinct genepools (Population Uganda A and Pop Ug B) were formed using molecular markers (18 SSR markers)
- Controlled crossing (inter- and intra-gene-pool) for population improvement and polycross crossing are in progress

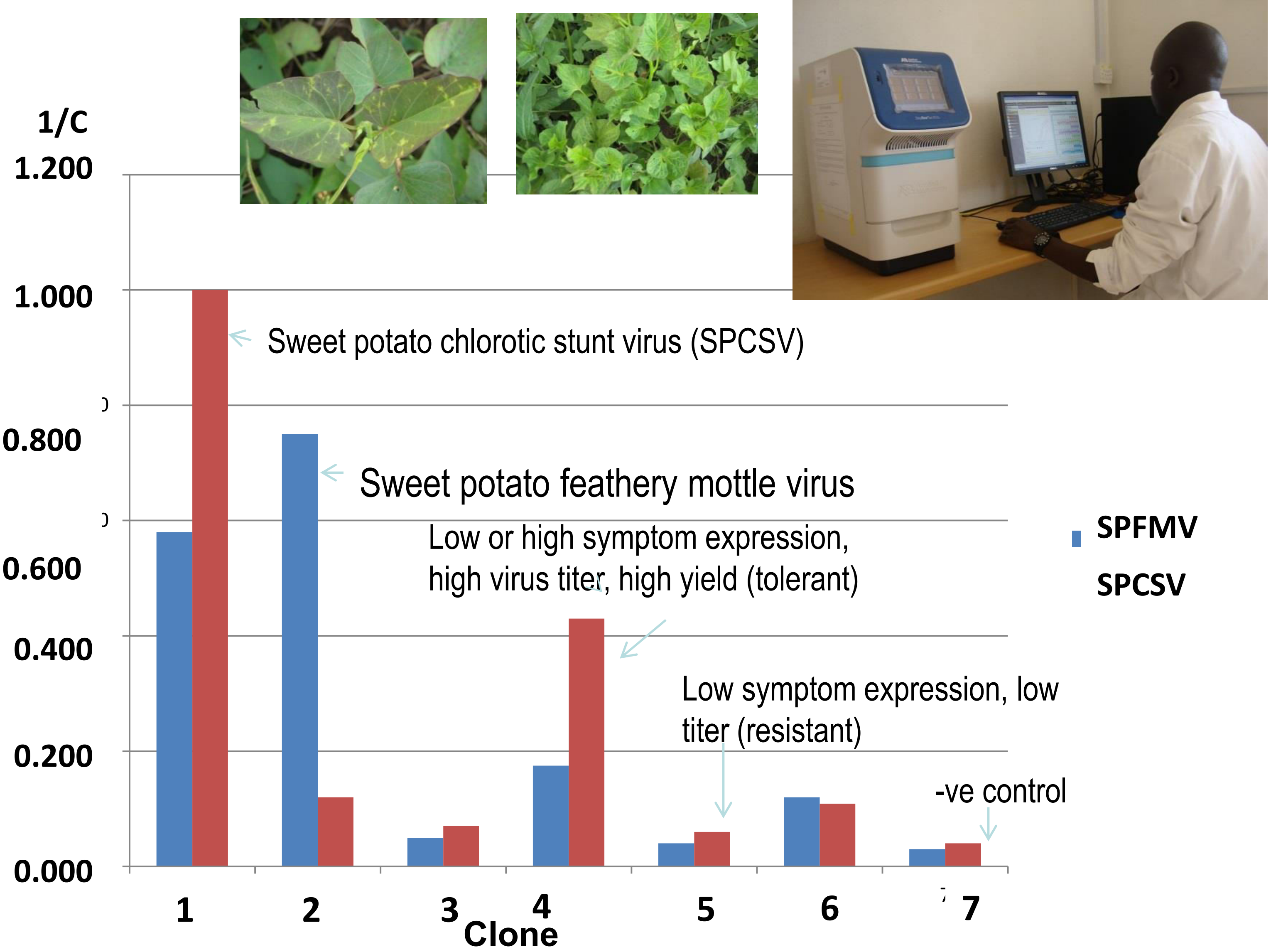




Pop Ug A

Pop Ug B

Field screening for SPVD resistance: choice of parents/large No's of progeny for field screening



Sweet potato chlorotic stunt virus (SPCSV)

Sweet potato feathery mottle virus

Low or high symptom expression, high virus titer, high yield (tolerant)

Low symptom expression, low titer (resistant)

-ve control

Discrimination of resistant and tolerant clones using real-time PCR (Ct = cycle threshold)

Virus accumulation in promising clones

Clone	Root yield (t/ha)	[1]SPVD (3 seasons)	Mean scores (3 reps, May-Aug 2012)		Class	SPFMV	SPCSV
			SPVD	Alternaria blight		[2](1/ΔCt)	(1/ΔCt)
4.3	5.1	3.3	1.3	2.0	Susceptible	0.556	1.011
17.3	6.1	2.0	1.0	1.7	**Resistant**	0.053	0.067
21.4	16.2	1.0	1.5	1.7	**Tolerant**	0.144	0.463
23.11	19.9	1.3	1.5	2.7	**Tolerant**	0.273	0.162
24.7	5.4	2.0	2.0	1.0	**Resistant**	0.053	0.053
29.3	7.0	3.3	2.5	1.7	Susceptible	0.052	0.349
NSP11	17.4	2.0	1.3	1.0	**Resistant**	0.113	0.064
Mean	10.7	2.1	1.6	1.7	**-ve control**	0.052	0.062
$LSD_{0.05}$	4.9	1.5	0.8	0.6			
CV (%)	27.3	29.8	35.1	39.6			

[1]SPVD = sweetpotato virus disease; SPFMV = *Sweet potato feathery mottle virus*; SPCSV = *Sweet potato chlorotic stunt virus*. [2]

[2]ΔCt = Delta Ct = Ct gene test – Ct endogenous control.

SPVD genotypes which show clear virus symptoms within first two months after planting are considered susceptible (mean score >3.0 on a 1-5 scale, 1= no symptoms, 5 = severe symptoms). NSP11 = NKA1081L = NASPOT 11

Can we make virus resistance breeding easier?

Thank you for your attention